

SEQUENCE LISTING

<110> CARLOCK, Leon
CYPHER, Maria

<120> Bioactive Peptides and Unique IRES Elements from
Myelin Proteolipid Protein PLP/DM20

<130> 2872-0010

<140> (not yet assigned)

<141> 2004-06-16

<150> PCT/US03/39873

<151> 2003-12-16

<150> US 60/433,573

<151> 2002-12-16

<160> 40

<170> PatentIn version 3.2

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<212> DNA

<213> Homo sapiens

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20 25 30	
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Cys Gly Cys Gly His Glu Ala Leu Thr Gly Thr Glu Lys Leu Ile Glu	
35 40 45	
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Thr Tyr Phe Ser Lys Asn Tyr Gln Asp Tyr Glu Tyr Leu Ile Asn Val	
50 55 60	
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Ile His Ala Phe Gln Tyr Val Ile Tyr Gly Thr Ala Ser Phe Phe Phe	
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Leu Tyr Gly Ala Leu Leu Leu Ala Glu Gly Phe Tyr Thr Thr Gly Ala	
85 90 95	

gtc agg cag atc ttt ggc gac tac aag acc acc atc tgc ggc aag ggc	336
Val Arg Gln Ile Phe Gly Asp Tyr Lys Thr Thr Ile Cys Gly Lys Gly	
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ctg agc gca acg gta aca ggg ggc cag aag ggg agg ggt tcc aga ggc	384
Leu Ser Ala Thr Val Thr Gly Gly Gln Lys Gly Arg Gly Ser Arg Gly	
115 120 125	
caa cat caa gct cat tct ttg gag cgg gtg tgt cat tgt ttg gga aaa	432
Gln His Gln Ala His Ser Leu Glu Arg Val Cys His Cys Leu Gly Lys	
130 135 140	
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Trp Leu Gly His Pro Asp Lys Phe Val Gly Ile Thr Tyr Ala Leu Thr	
145 150 155 160	
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Val Val Trp Leu Leu Val Phe Ala Cys Ser Ala Val Pro Val Tyr Ile	
165 170 175	
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Tyr Phe Asn Thr Trp Thr Thr Cys Asp Ser Ile Ala Phe Pro Ser Lys	
180 185 190	
acc tct gcc agt ata ggc agt ctc tgt gct gac gcc aga atg tat ggt	624
Thr Ser Ala Ser Ile Gly Ser Leu Cys Ala Asp Ala Arg Met Tyr Gly	
195 200 205	
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210 215 220	
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225 230 235 240	
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245 250 255	
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35      40      45

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50      55      60

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100     105     110

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165     170     175

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195     200     205

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210     215     220

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Cys Gly Cys Gly His Glu Ala Leu Thr Gly Thr Glu Lys Leu Ile Glu
35 40 45
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Thr Tyr Phe Ser Lys Asn Tyr Gln Asp Tyr Glu Tyr Leu Ile Asn Val
50 55 60
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Ile His Ala Phe Gln Tyr Val Ile Tyr Gly Thr Ala Ser Phe Phe Phe
65 70 75 80
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Leu Tyr Gly Ala Leu Leu Leu Ala Glu Gly Phe Tyr Thr Thr Gly Ala
85 90 95
gtc agg cag atc ttt ggc gac tac aag acc acc atc tgc ggc aag ggc 336
Val Arg Gln Ile Phe Gly Asp Tyr Lys Thr Thr Ile Cys Gly Lys Gly
100 105 110
ctg agc gca acg ttt gtg ggc atc acc tat gcc ctg acc gtt gtg tgg 384
Leu Ser Ala Thr Phe Val Gly Ile Thr Tyr Ala Leu Thr Val Val Trp
115 120 125
ctc ctg gtg ttt gcc tgc tct gct gtg ccc gtg tac att tac ttc aac 432
Leu Leu Val Phe Ala Cys Ser Ala Val Pro Val Tyr Ile Tyr Phe Asn
130 135 140
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Thr Trp Thr Thr Cys Asp Ser Ile Ala Phe Pro Ser Lys Thr Ser Ala
145 150 155 160
agt ata ggc agt ctc tgt gct gac gcc aga atg tat ggt gtt ctc cca 528
Ser Ile Gly Ser Leu Cys Ala Asp Ala Arg Met Tyr Gly Val Leu Pro
165 170 175
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Trp Asn Ala Phe Pro Gly Lys Val Cys Gly Ser Asn Leu Leu Ser Ile
180 185 190

tgc aaa aca gct gag ttc caa atg acc ttc cac ctg ttt att gct gca	624
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35 40 45

Thr Tyr Phe Ser Lys Asn Tyr Gln Asp Tyr Glu Tyr Leu Ile Asn Val
50 55 60

Ile His Ala Phe Gln Tyr Val Ile Tyr Gly Thr Ala Ser Phe Phe Phe
65 70 75 80

Leu Tyr Gly Ala Leu Leu Leu Ala Glu Gly Phe Tyr Thr Thr Gly Ala
85 90 95

Val Arg Gln Ile Phe Gly Asp Tyr Lys Thr Thr Ile Cys Gly Lys Gly
100 105 110

Leu Ser Ala Thr Phe Val Gly Ile Thr Tyr Ala Leu Thr Val Val Trp
115 120 125

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130 135 140

Thr Trp Thr Thr Cys Asp Ser Ile Ala Phe Pro Ser Lys Thr Ser Ala
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165 170 175

Trp Asn Ala Phe Pro Gly Lys Val Cys Gly Ser Asn Leu Leu Ser Ile
 180 185 190
 Cys Lys Thr Ala Glu Phe Gln Met Thr Phe His Leu Phe Ile Ala Ala
 195 200 205
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 Ser Asn Leu Leu Ser Ile Cys Lys Thr Ala Glu Phe Gln Met Thr Phe
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 cac ctg ttt att gct gca ttt gtg ggg gct gca gct aca ctg gtt tcc 144
 His Leu Phe Ile Ala Ala Phe Val Gly Ala Ala Ala Thr Leu Val Ser
 35 40 45
 ctg ctc acc ttc atg att gct gcc act tac aac ttt gcc gtc ctt aaa 192
 Leu Leu Thr Phe Met Ile Ala Ala Thr Tyr Asn Phe Ala Val Leu Lys
 50 55 60
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Leu Val Ser Leu Leu Thr Phe Met Ile Ala Ala Thr Tyr Asn Phe Ala
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Val Cys Gly Ser Asn Leu Leu Ser Ile Cys Lys Thr Ala Glu Phe Gln
15 20 25

atg acc ttc cac ctg ttt att gct gcg ttt gtg ggt gct gcg gcc aca 145
Met Thr Phe His Leu Phe Ile Ala Ala Phe Val Gly Ala Ala Ala Thr
30 35 40 45

cta gtt tcc ctg ctc acc ttc atg att gct gcc act tac aac ttc gcc 193
Leu Val Ser Leu Leu Thr Phe Met Ile Ala Ala Thr Tyr Asn Phe Ala
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 Val Cys Gly Ser Asn Leu Leu Ser Ile Cys Lys Thr Ala Glu Phe Gln
 15 20 25
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 30 35 40 45
 cta gtt tcc ctg ctc acc ttc atg att gct gcc act tac aac ttc gcc 193
 Leu Val Ser Leu Leu Thr Phe Met Ile Ala Ala Thr Tyr Asn Phe Ala
 50 55 60
 gtc ctt aaa ctc atg ggc cga ggc acc aag ttc cat cat cac cat cac 241
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 35 40 45
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 50 55 60
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 Ala Ala Thr Leu Val Ser Leu Leu Thr Phe Met Ile Ala Ala Thr Tyr
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 Ala Ala Thr Leu Val Ser Leu Leu Thr Phe Met Ile Ala Ala Thr Tyr
 15 20 25

aac ttc gcc gtc ctt aaa ctc atg ggc cga ggc acc aag ttc cat cat 145
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His His His His

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Val Cys Gly Cys Cys Gly His Thr Ser Phe Pro Ala His Leu His Asp
15 20 25

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